FIG. 1A

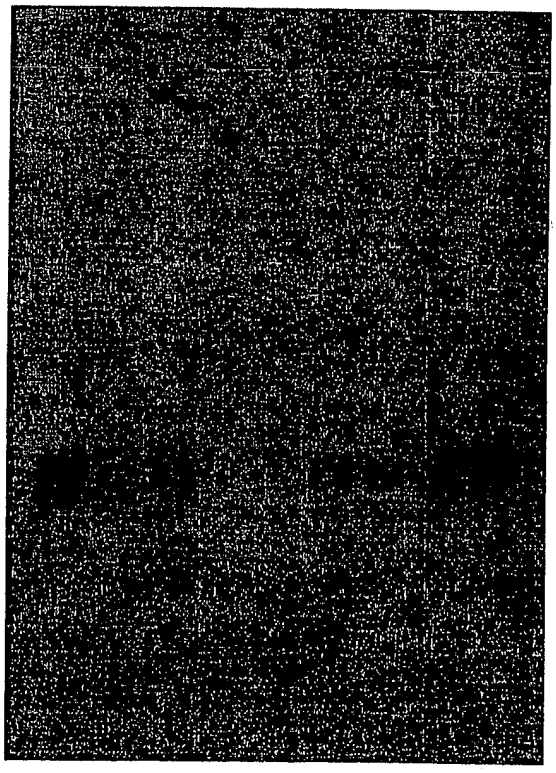


FIG.1B

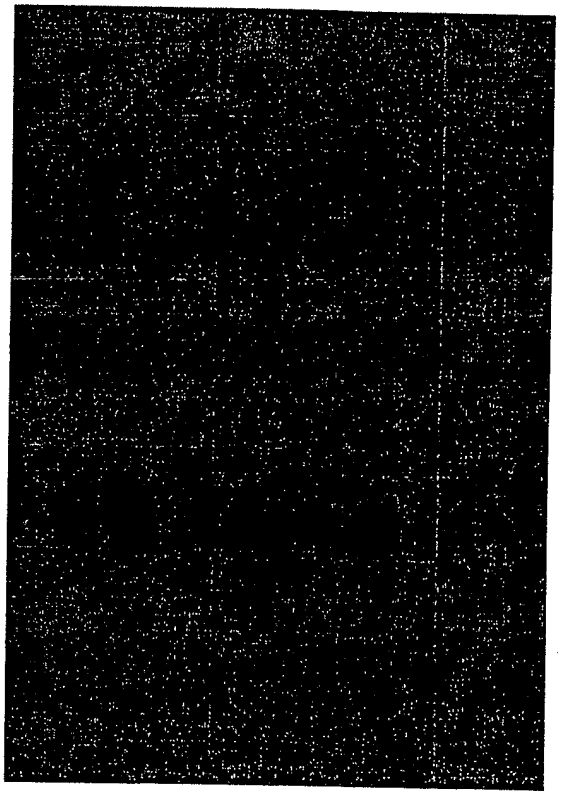


FIG. 2

```
   1          CTGGCTGCTGTGGAGTTTGTGACATACTAGGTGACACCCTTGGAGTCACTTC
  53 TCTTCAACTCCAGCTTAGAAGTGCCTGCCTGGCTCAGGGTCTGCACTGCAGCCTACTCCT
 113 TGCTTCAGGGCCTGACTGCAACGCCAAAGCCTATCCTATAGCGGCAGCGCCAGCAGCCAC
 173 TCAAACCAGCCACAGCTCCCCGGCAACCGAACCATGAACACCGAAATGTATCAGACCCCC
                                        MetAsnThrGluMetTyrGlnThrPro

 233 ATGGAGGTGGCGGTCTATCAGCTGCACAATTTCTCCACCTCCTTCTTTTCTTCTCTGCTT
     MetGluValAlaValTyrGlnLeuHisAsnPheSerThrSerPhePheSerSerLeuLeu

 293 GGAGGGGATGTGGTTTCCGTTAAACTGGATAACAGTGCCTCCGGAGCCAGTGTGGTGGCC
     GlyGlyAspValValSerValLysLeuAspAsnSerAlaSerGlyAlaSerValValAla

 353 CTAGACAACAAGATTGAGCAGGCCATGGACCTCGTGAAGAACCACCTGATGTACGCTGTG
     LeuAspAsnLysIleGluGlnAlaMetAspLeuValLysAsnHisLeuMetTyrAlaVal

 413 AGAGAGGAGGTGGAGGTCCTAAAGGAGCAGATTCGTGAGCTGCTTGAGAAGAACTCCCAG
     ArgGluGluValGluValLeuLysGluGlnIleArgGluLeuLeuGluLysAsnSerGln

 473 CTGGAGCGCGAGAACACCCTCCTGAAGACGCTGGCAAGCCCCGAGCAACTGGAAAAGTTC
     LeuGluArgGluLeuThrLeuLeuLysThrLeuAlaSerProGluGlnLeuGluLysPhe

 533 CAGTCCCGGCTGAGCCCTGAAGAGCCAGCACCTGAAGCCCCAGAAACCCCGGAAACCCCG
     GlnSerArgLeuSerProGluGluProAlaProGluAlaProGluThrProGluThrPro

 593 GAAGCCCCTGGTGGTTCTGCGGTGTAAGTGGCTCTGTCCTTAGGGTGGGCAGAGCCACAT
     GluAlaProGlyGlySerAlaVal *

 653 CTTGTTCTACCTAGTTCTTTCCAGTTTGTTTTTGGCTCCCCAAGGGTCATCTCATGTGGA
 713 GAACTTTACACCTAACATAGCTGGTGCCAAGAGATGTCCCAAGGACATGCCCATCTGGGT
 773 CCACTCCAGTGACAGACCCCTGACAAAGAGCAGGTCTCTGGAGACTAAGTTGCATGGGGC
 833 CTAGTAACACCAAGCCAGTGAGCCTGTCGTGTCACCGGGCCCTGGGGGCTCCCAGGGCTG
 893 GGCAACTTAGTTACAGCTGACCAAGGAGAAAGTAGTTTTGAGATGTGATGCCAGTGTGCT
 953 CCAGAAAGTGTAAGGGGTCTGTTTTTCATTTCCATGGACATCTTCCACAGCTTCACCTGA
1013 CAATGACTGTTCCTATGAAGAAGCCACTTGTGTTCTAAGCAGAAGCAACCTCTCTCTTCT
1073 TCCTCTGTCTTTTCCAGGCAGGGGCAGAGATGGGAGAGATTGAGCCAAATGAGCCTTCTG
1113 TTGGTTAATACTGTATAATGCATGGCTTTGTGCACAGCCCAGTGTGGGGTTACAGCTTTG
1193 GGATGACTGCTTATAAAGTTCTGTTTGGTTAGTATTGGCATCGTTTTTCTATATAGCCAT
1253 AATGCGTATATATACCCATAGGGCTAGATCTATATCTTAGGGTAGTGATGTATACATATA
1313 CACATACACCTACATGTTGAAGGGCCTAACCAGCTTTGGGAGTACTGACTGGTCTCTTAT
1373 CTCTTAAAGCTAAGTTTTTGACTGTGCTAATTTACCAAATTGATCCAGTTTGTCCTTTAG
1433 ATTAAATAAGACTCGATATGAGGGAGGGAGGGGAAGACCAGCCTCACAATGCGGCCACAG
1493 ATGCCTTGCTGCTGCAGTCCTCCCTGATCTGTCCACTGAAGACATGAAGTCCTCTTTTGA
1553 ATGCCAAACCCACCATTCATTGGTGCTGACTACATAGAATGGGGTTGAGAGAAGATCAGT
1613 TTGGACTTCACATTTTGTTTTAAGTTTTAGGTTGTTTTTTTTTGGTTTTGTTTGTTTGT
1673 TTGTTTGTTTGTTTTTGTTTTTTGTTTTTCTTTTTTAAGTTCTTGTGGGGAAACTTTGGG
1733 GTTAATCAAAGGATGTAGTCCTGTGGTAGACCAGAGGAGTAACTAGTTTTGATCCTTTGG
1793 GGTGTGGAAAATGTACCCAGGAAGCTTGTGTAAGGAGGTTCTGTGACAGTGAACACTTTC
1853 CACTTTCTGACACCTCATCCTGCTGTACGACTCCAGGATTTGGATTTGGATTTTTCAAAT
```

FIG.3A

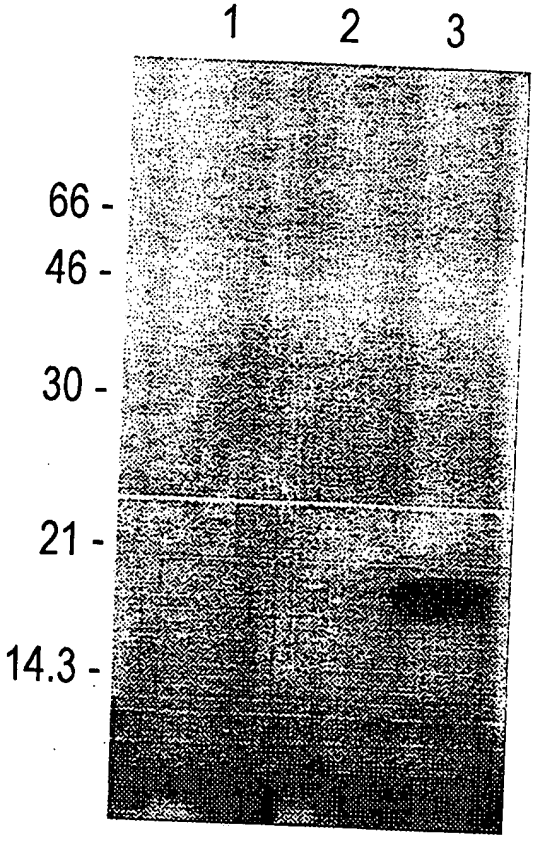


FIG. 3B

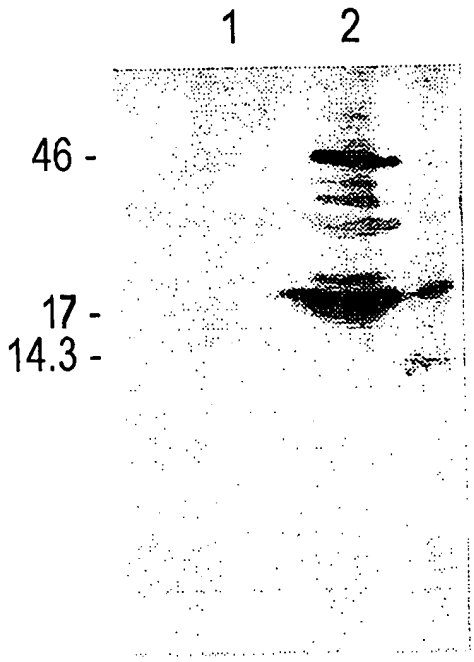
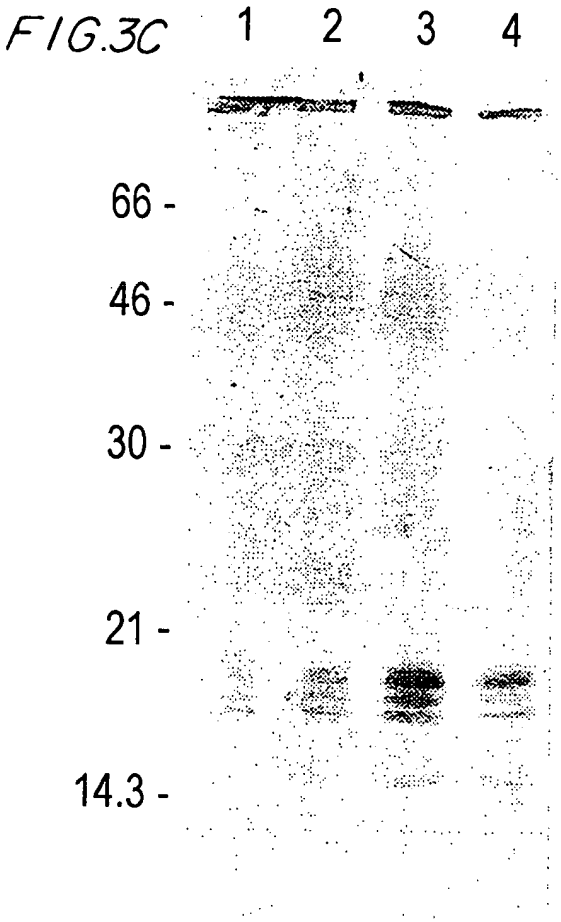


FIG.3C



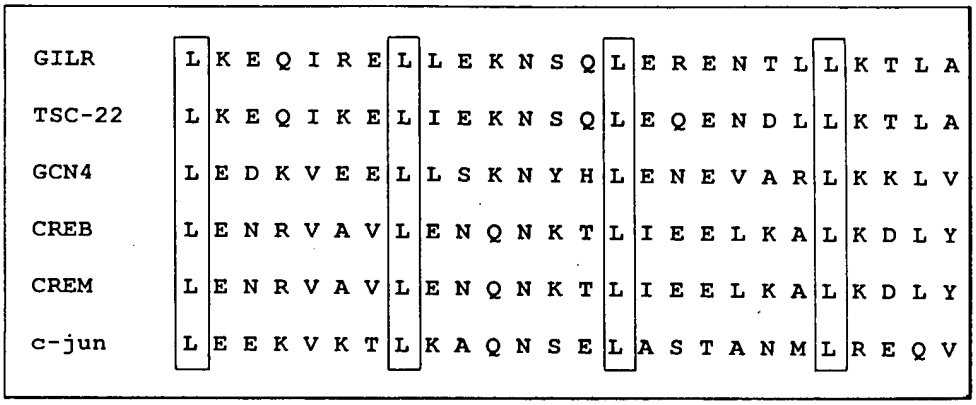


FIG. 4

FIG.5A

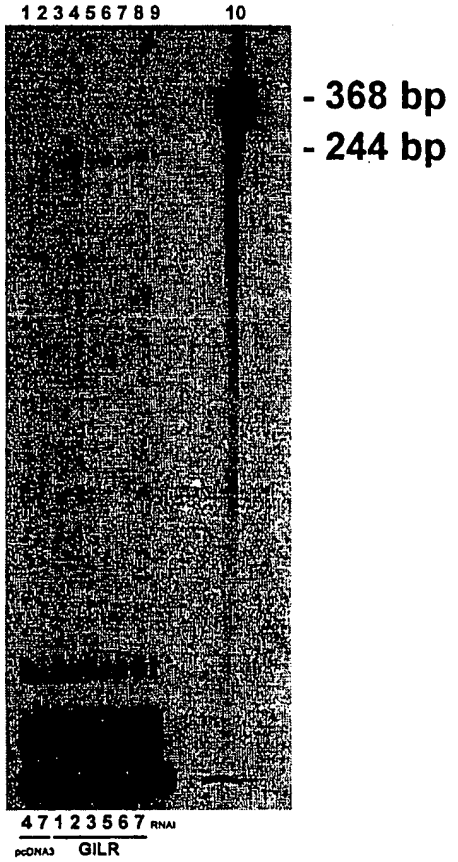


FIG.5B

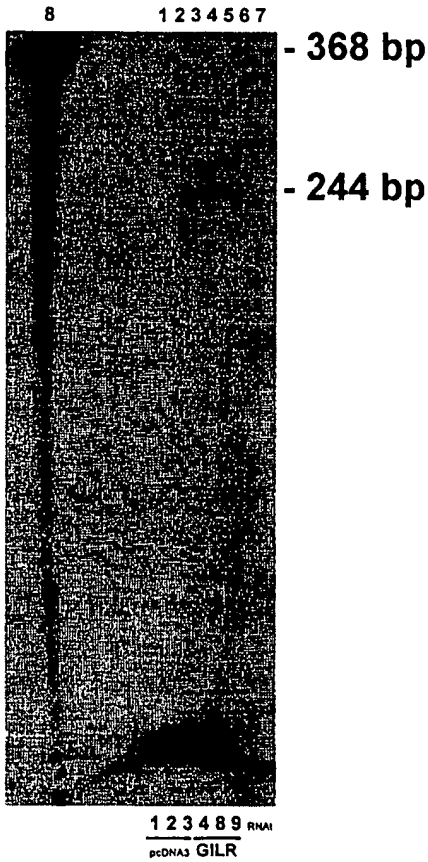


FIG.5C

FIG. 6

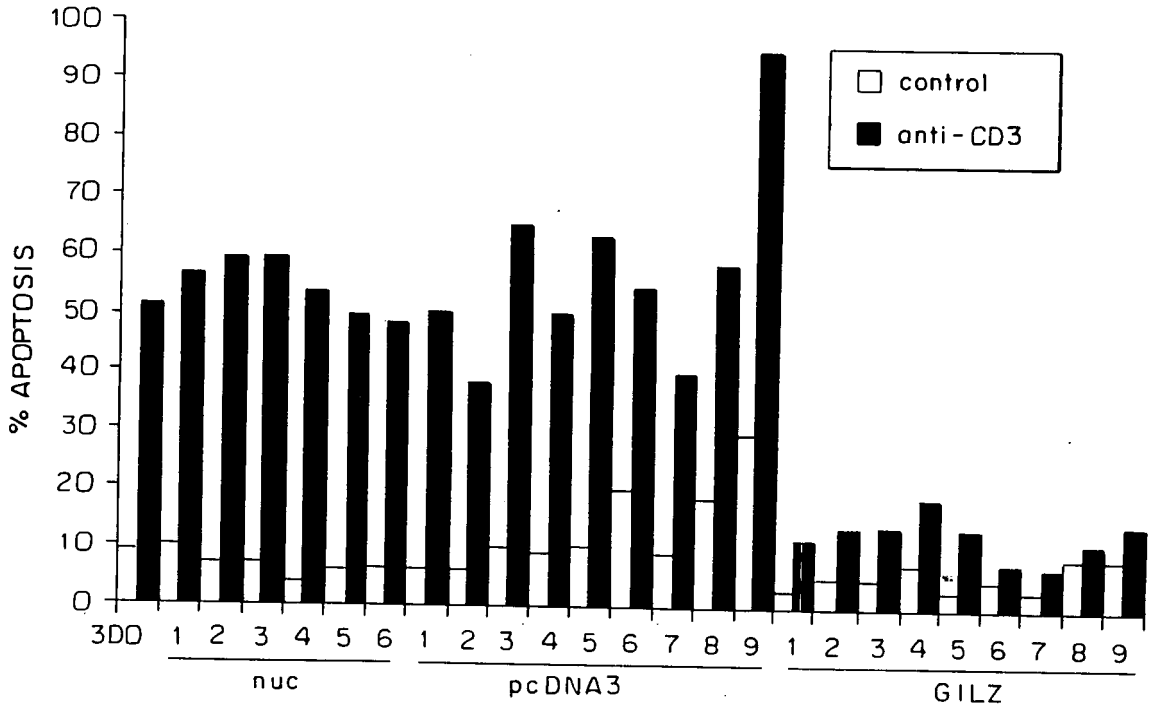


FIG. 7A

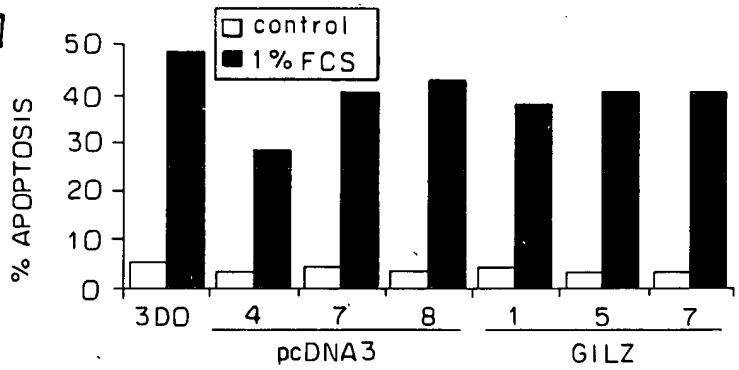


FIG. 7B

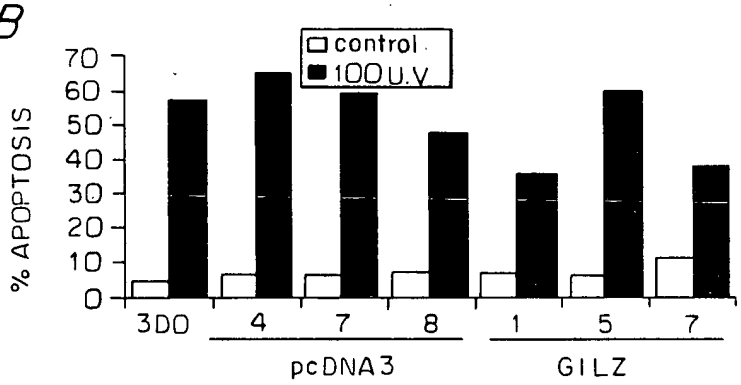


FIG. 7C

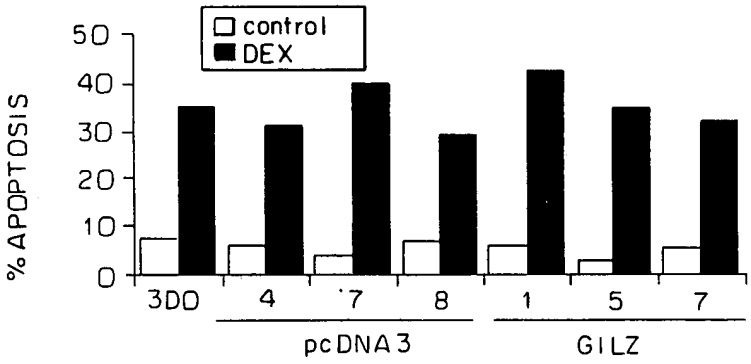


FIG. 7D

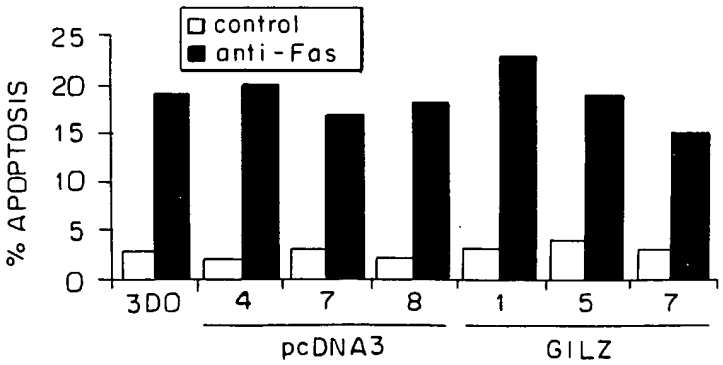


FIG. 8A

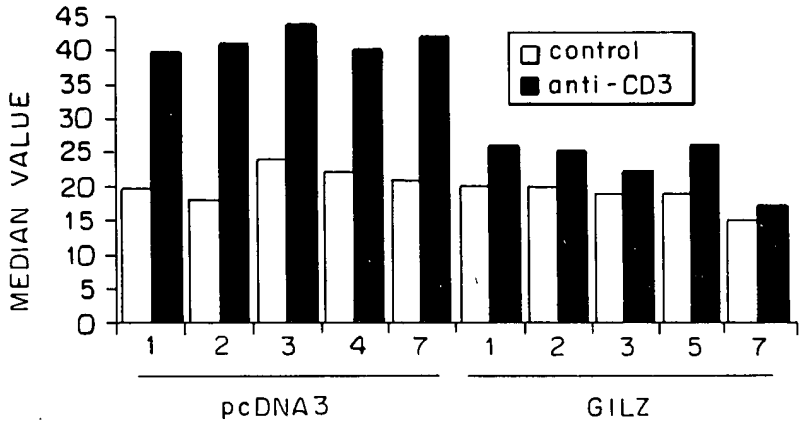


FIG. 8B

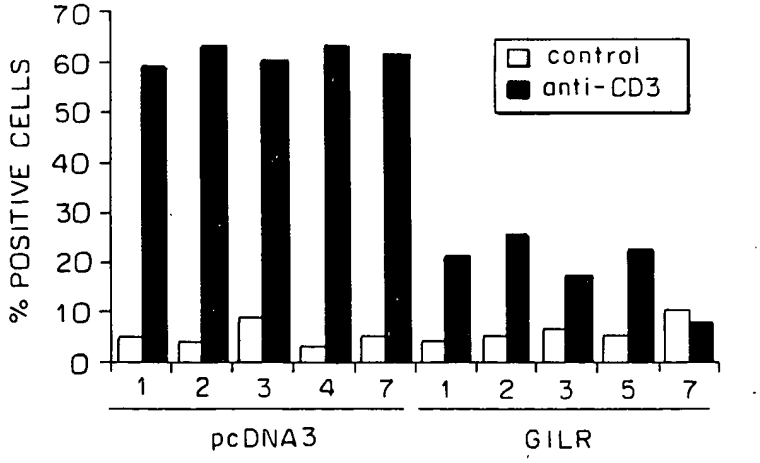


FIG. 9A

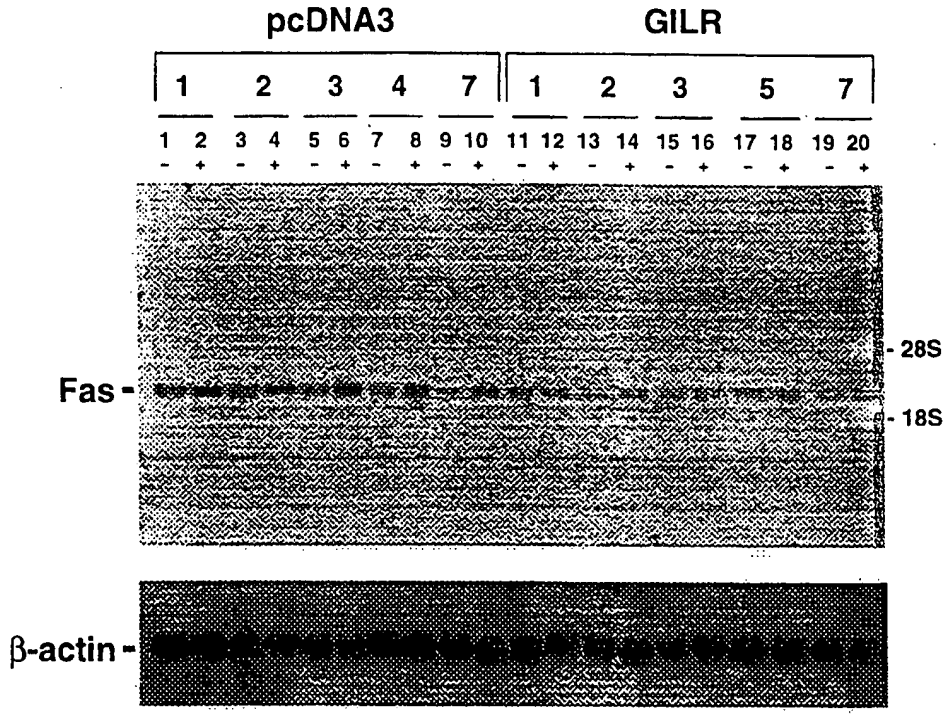


FIG. 9B

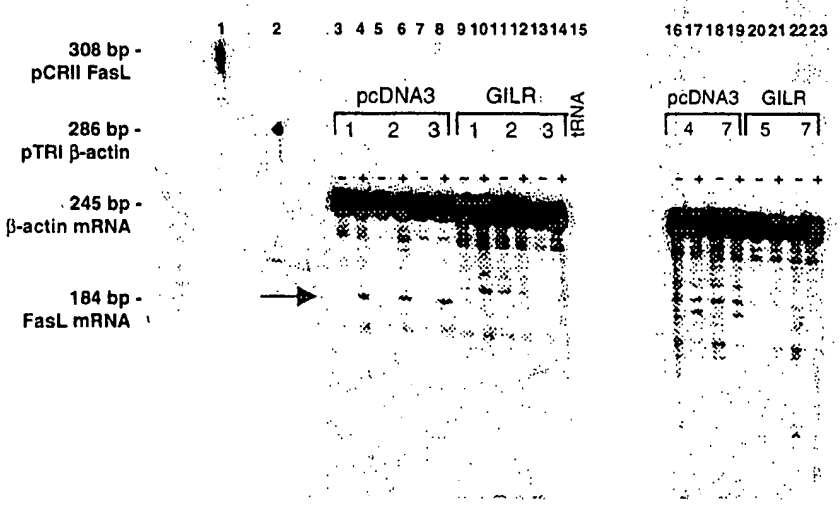


FIG.10A

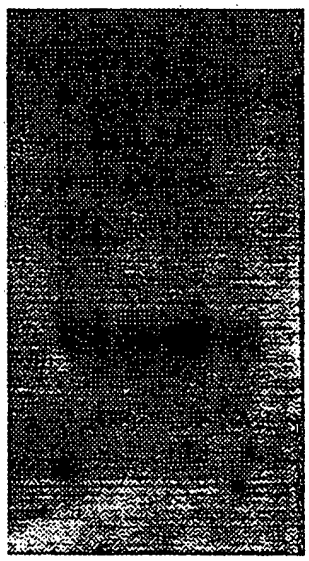


FIG.10B

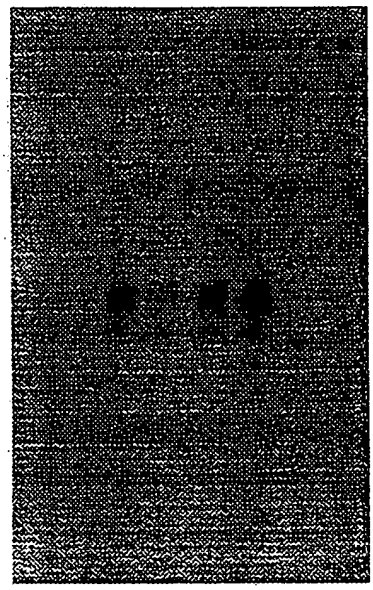


FIG. 11A

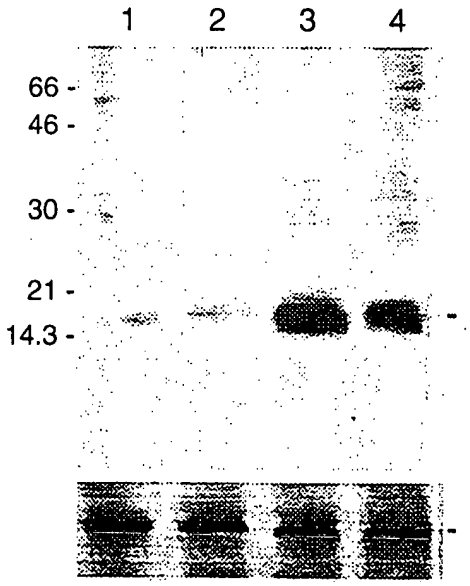


FIG. 11B

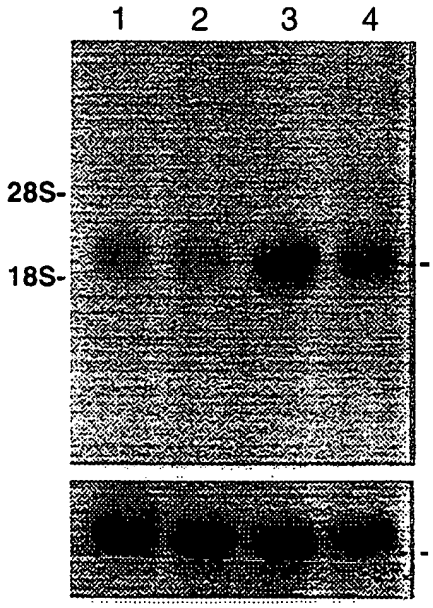


FIG.12A

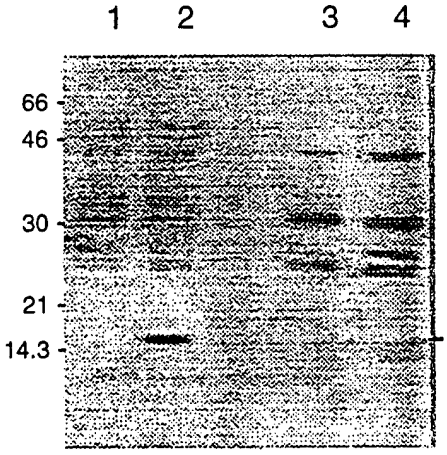


FIG.12B

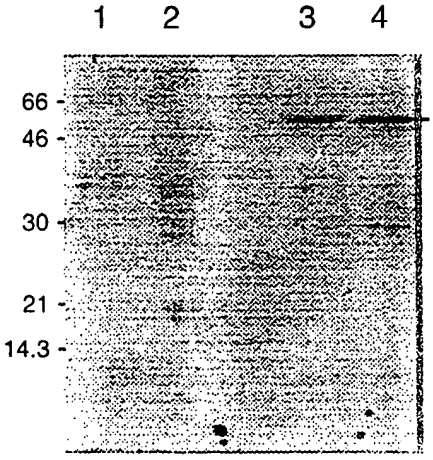


FIG. 13

```
   1 AATTCGGGGGCCGTGGAGTTTGTGACATACGAGGTGACACCCCTCGAGTCACTTCCCTTC
  61 AACTCCAGCTGGAGCGCCTGCTTGGCTTTGGGTTCGTTCTGCAGCCTTCGCCCCCGCTCCT
 121 AGCCTCAGGGCCGGACTCCAGCGCAGAGCCCAGCCCAGCGCAGCCTGCCAGCAGCCACCC
 181 AGCCGCCCAGCCGCCCAGCCCCGCACGAAACCCGGCCAGAGCTTCCTAGCAGCCCGAGCC
 241 ATGAACACCGAAATGTATCAGACCCCCATGGAGGTGGCGGTCTACCAGCTGCACAATTTC
     MetAsnThrGluMetTyrGlnThrProMetGluValAlaValTyrGlnLeuHisAsnPhe

 301 TCCATCTCCTTCTTCTCTTCTCTGCTTGGAGGGGATGTGGTTTCCGTTAAGCTGGACAAC
     SerIleSerPhePheSerSerLeuLeuGlyGlyAspValValSerValLysLeuAspAsn

 361 AGTGCCTCCGGAGCCAGCGTGGTGGCCATAGACAACAAGATCGAACAGGCCATGGATCTG
     SerAlaSerGlyAlaSerValValAlaIleAspAsnLysIleAspGlnAlaMetAspLeu

 421 GTGAAGAATCATCTGATGTATGCTGTGAGAGAGGAGGTGGAGATCCTGAAGGAGCAGATC
     ValLysAsnHisLeuMetTyrAlaValArgGluGluValGluIleLeuLysGluGlnIle

 481 CGAGAGCTGGTGGAGAAGAACTCCCAGCTAGAGCGTGAGAACACCCTGTTGAAGACCCTG
     ArgGluLeuValGluLysAsnSerGlnLeuGluArgGluAsnThrLeuLeuLysThrLeu

 541 GCAAGCCCAGAGCAGCTGGAGAAGTTCCAGTCCTGTCTGAGCCCTGAAGAGCCAGCTCCC
     AlaSerProGluGlnLeuGluLysPheGlnSerCysLeuSerProGluGluProAlaPro

 601 GAATCCCCACAAGTGCCCGAGGCCCCTGGTGGTTCTGCGGTGTAAGTGGCTCTGTCCTCA
     GluSerProGlnValProGluAlaProGlyGlySerAlaVal *

 661 GGGTGGGCAGAGCCACTAAACTTGTTTTACCTAGTTCTTTCCAGTTTGTTTTTGGCTCCC
 721 CAAGCATCATCTCACGAGGAGAACTTTACACCTAGCACAGCTGGTGCCAAGAGATGTCCT
 781 AAGGACATGGCCACCTGGGTCCACTCCAGCGACAGACCCCTGACAAGAGCAGGTCTCTGG
 841 AGGCTGAGTTGCATGGGGCCTAGTAACACCAAGCCAGTGAGCCTCTAATGCTACTGCGCC
 901 CTGGGGGCTCCCAGGGCCTGGGCAACTTAGCTGCAACTGGCAAAGGAGAAGGGTAGTTTG
 961 AGGTGTGACACCAGTTTGCTCCAGAAAGTTTAAGGGGTCTGTTTCTCATCTCCATGGACA
1021 TCTTCAACAGCTTCACCTGACAACGACTGTTCCTATGAAGAAGCCACTTGTGTTTTAAGC
1081 AGAGGCAACCTCTCTCTTCTCCTCTGTTTCGTGAAGGCAGGGGACACAGATGGGAGAGAT
1141 TGAGCCAAGTCAGCCTTCTGTTGGTTAATATGGTATAATGCATGGCTTTGTGCACAGCCC
1201 AGTGTGGGATTACAGCTTTGGGATGACCGCTTACAAAGTTCTGTTTGGTTAGTATTGGCA
1261 TAGTTTTTCTATATAGCCATAAATGCGTATATATACCCATAGGGCTAGATCTGTATCTTA
1321 GTGTAGCGATGTATACATATACACATCCACCTACATGTTGAAGGGCCTAACCAGCCTTGG
1381 GAGTATTGACTGGTCCCTTACCTCTTATGGCTAAGTCTTTGACTGTGTTCATTTACCAAG
1441 TTGACCCAGTTTGTCTTTTAGGTTAAGTAAGAACTCGAGAGTAAAGGCAAGGAGGGGGGC
1501 CAGCCTCTGAATGCGGCCACGGATGCCTTGCTGCTGCAACCCTTTCCCCAGCTGTCCACT
1561 GAAACGTGAAGTCCTGTTTTGAATGCCAAACCCACCATTCACTGGTGCTGACTACATAGA
1621 ATGGGTTGAGAGAAGATCAGTTTGGGCTTCACAGTGTCATTTGAAAAAGCGTTTTTGTTT
1681 TGTTTTGAATTATTGTGGAAAACTTTCAAGTGAACAGAAGGATGGTGTCCTACTGTGGAT
1741 GAGGGATGAACAAGGGGATGGCTTTGATCCAATGGAGCCTGGGAGGTGTGCCCAGAAAGC
1801 TTGTCTGTAGCGGGTTTTGTGAGAGTGAACACTTTCCACTTTTTGACACCTTATCCTGAT
1861 GTATGGTTCCAGGATTTGGATTTTGATTTTCCAAATGTAGCTTGAAATTTCAATAAACTT
1921 TGCTCTGTTTTTTCTAAAAAATAAAAA
```

FIG. 14A

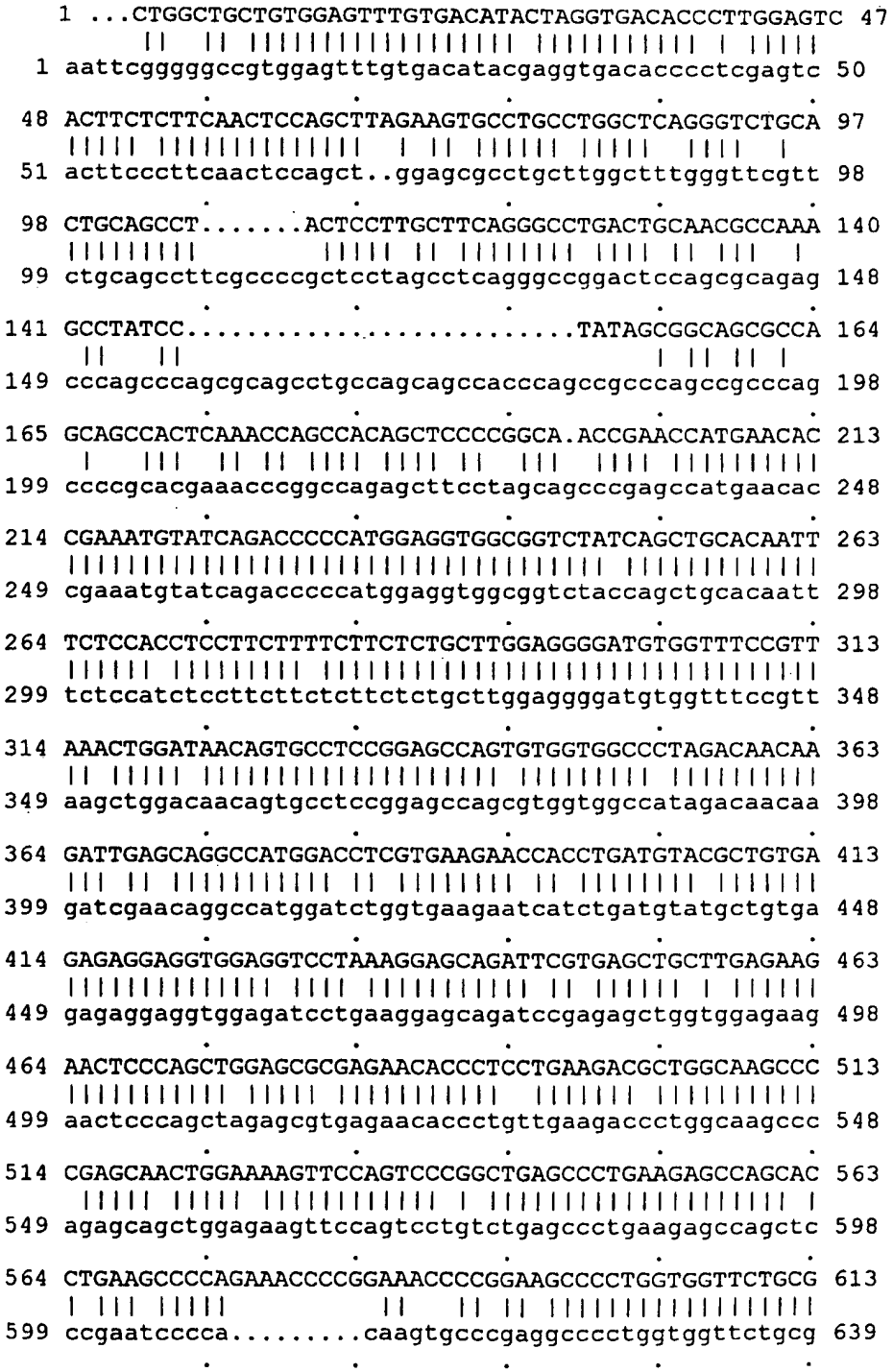


FIG. 14B

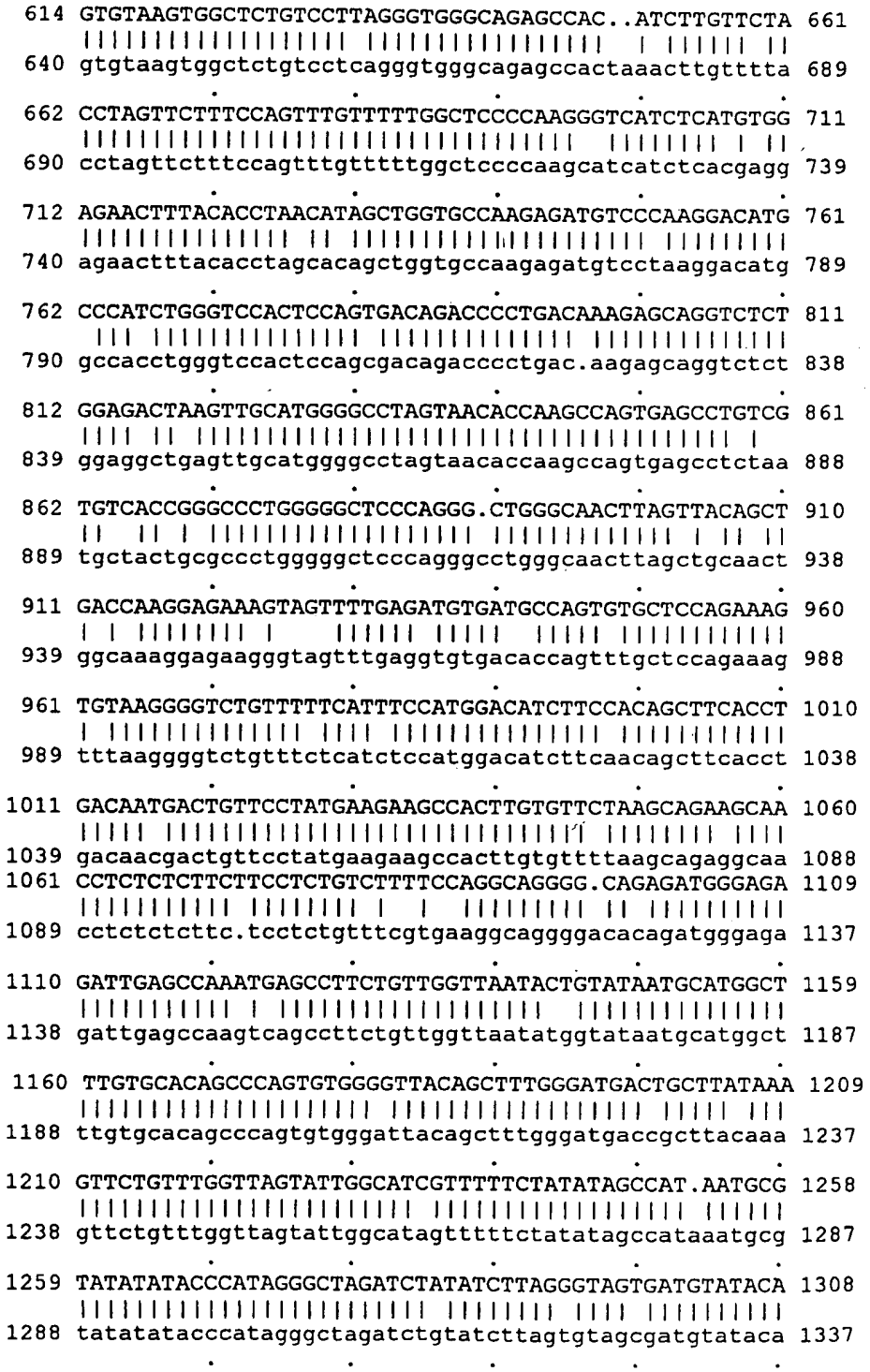


FIG. 14C

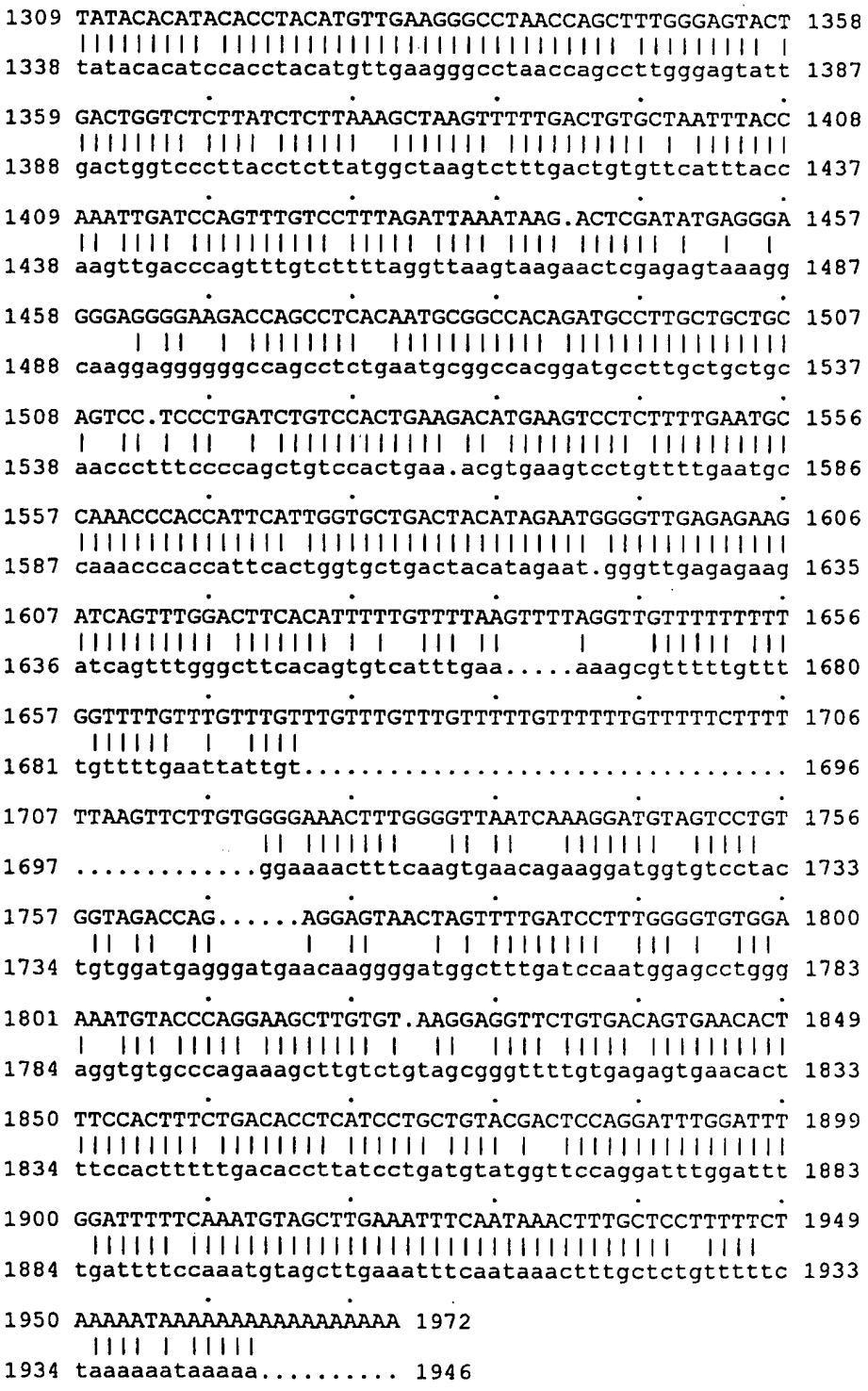


FIG. 15

```
mG     1 MNTEMYQTPMEVAVYQLHNFSTSFFSSLLGGDVVSVKLDNSASGASVVAL  50

hG     1 MNTEMYQTPMEVAVYQLHNFSISFFSSLLGGDVVSVKLDNSASGASVVAI  50
         ==================== ============================-

hT     2 KSQWCRPVAMDLGVYQLRHFSISFLSSLLGTENASVRLDNSSSGASVVAI  51
                  =---====  == == ===== -  ==-=====-========

mG    51 DNKIEQAMDLVKNHLMYAVREEVEVLKEQIRELLEKNSQLERENTLLKTL 100

hG    51 DNKIEQAMDLVKNHLMYAVREEVEILKEQIRELVEKNSQLERENTLLKTL 100
         ========================-========-================

hT    52 DNKIEQAMDLVKSHLMYAVREEVEVLKEQIKELIEKNSQLEQENNLLKTL 101
         ============ ==================-==-=======-== =====

hD     1        MDLVKNHLMYAVREEVEILKEQIRELVEKNSQLERENTLLKTL  43
                  ================-========-=======-========

mG   101 ASPEQLEKFQSRLSPEEPAPEAPETPETPEAPGGSAV*              137

hG   101 ASPEQLEKFQSCLSPEEPAPES...PQVPEAPGGSAV*             134
         ========== =========-    =- =========

hT   102 ASPEQLAQFQAQLQTGSPPATTQPQGTTQPPAQPASQGSGPTA*       144
         ====== -==- =    =    -      =

hD    44 ASPEQLEKFQSCLSPEEPAPES...PQVPEAPGGSAV*              77
         =======-=== =========-    ===========
```